Amendments to the Specification:

Please replace the paragraph on page 1, lines 8-9 with the following amended paragraph:

The current application claims the benefit of U.S. Provisional Application No. 60/259,502, filed January 2, 2001, and now abandoned, which is herein incorporated by reference.

Please replace at paragraph at page 16, line 29 bridging to page 17, line 22 with the following amended paragraph:

A preferred example of algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al., Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al., J. Mol. Biol.* 215:403-410 (1990), respectively. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information ~~(http://www.ncbi.nlm.nih.gov/)~~. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al., supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the

cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Please replace at paragraph at page 25, lines 23-31 with the following amended paragraph:

In preferred embodiments, a ~~TaqMan~~ TAQMAN® based assay is used to quantify Pellino 1 or 2 polynucleotides. ~~TaqMan~~ TAQMAN® based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, *e.g.*, ~~AmpliTaq~~ AMPLITAQ®, results in the cleavage of the ~~TaqMan~~ TAQMAN® probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (*see*, for example, literature provided by Perkin-Elmer~~, *e.g.*, www2.perkin-elmer.com~~).

Please replace at paragraph at page 35, lines 2-9 with the following amended paragraph:

The present methods can be used to diagnose and treat any of a number of types of cancers. In preferred embodiments, cancers such as epithelial-derived cancers will be diagnosed and/or treated, *e.g.*, lung, colon, and ovarian cancer. Other epithelial cancers include, *e.g.*, breast, kidney, stomach, bladder, and colorectal cancers. A cancer at any stage of

progression can be detected, such as primary, metastatic, and recurrent cancers. Information regarding numerous types of cancer can be found, *e.g.*, from the American Cancer Society ~~(www3.cancer.org)~~, or from, *e.g.*, Wilson *et al.* (1991) Harrison's Principles of Internal Medicine, 12th Edition, McGraw-Hill, Inc.